

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 09:12:48 ; Search time 48 Seconds
(without alignments)
769.917 Million cell updates/sec

Title: US-10-661-378-9

Perfect score: 2360

Sequence: 1 MEGGWPARGALLCLTVSLL.....RLVLLFWASSILTVIVLWNT 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2360	100.0	447	2	US-09-388-349-9
2	717.5	30.4	457	2	US-09-579-250-4
3	583.5	24.7	470	2	US-09-579-250-6
4	529.5	22.4	441	2	US-09-061-154-2
5	526.5	22.3	441	2	US-09-061-154-4
6	422.5	17.9	497	1	US-08-278-6358-5
7	422.5	17.9	497	2	US-08-464-2588-5
8	422.5	17.9	497	2	US-08-471-961-5
9	422.5	17.9	497	2	US-09-345-109C-5
10	419	17.8	504	2	US-08-660-451A-4
11	417.5	17.7	479	1	US-08-278-6358-2
12	417.5	17.7	479	2	US-08-464-2588-2
13	417.5	17.7	479	2	US-08-471-961-2
14	417.5	17.7	479	2	US-09-345-109C-2
15	415.5	17.6	494	2	US-08-487-596-10
16	415.5	17.6	494	2	US-08-484-722-2
17	415.5	17.6	494	2	US-08-660-451A-10
18	415.5	17.6	494	2	US-09-703-951A-10
19	412.5	17.5	502	2	US-09-579-250-14
20	407.5	17.3	502	2	US-09-579-250-10
21	405.5	17.2	510	1	US-08-278-6358-4
22	405.5	17.2	510	2	US-08-471-961-4
23	405.5	17.2	510	2	US-09-345-109C-4
24	405	17.2	458	2	US-08-487-596-16
25	405	17.2	458	2	US-08-484-722-4
26	405	17.2	458	2	US-09-703-951A-16
27	404.5	17.1	502	2	US-09-579-250-12

28	404.5	17.1	511	2	US-08-464-2588-4	Sequence 4, Appli
29	404	17.1	458	2	US-08-660-451A-16	Sequence 16, Appl
30	404	17.1	458	2	US-09-949-016-5986	Sequence 5986, Ap
31	402.5	17.1	529	1	US-08-496-855A-2	Sequence 2, Appli
32	402.5	17.1	529	2	US-08-487-596-2	Sequence 2, Appli
33	402.5	17.1	529	2	US-08-660-451A-2	Sequence 2, Appli
34	402.5	17.1	529	2	US-09-703-951A-2	Sequence 2, Appli
35	401	17.0	629	1	US-08-278-6358-6	Sequence 6, Appli
36	401	17.0	629	2	US-08-471-961-6	Sequence 6, Appli
37	401	17.0	629	2	US-09-345-109C-6	Sequence 6, Appli
38	400.5	17.0	607	2	US-09-949-016-7817	Sequence 7817, Ap
39	400.5	17.0	627	2	US-08-660-451A-6	Sequence 6, Appli
40	399.5	16.9	502	1	US-08-466-589-8	Sequence 8, Appli
41	399.5	16.9	502	1	US-08-700-636-8	Sequence 8, Appli
42	399.5	16.9	502	2	US-08-467-574-8	Sequence 8, Appli
43	399.5	16.9	502	2	US-09-217-345-8	Sequence 8, Appli
44	399.5	16.9	502	2	US-08-487-596-12	Sequence 12, Appli
45	399.5	16.9	502	2	US-09-892-985-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-388-349-9

; Sequence 9, Application US/09388349

; Patent No. 6365370

; GENERAL INFORMATION:

; APPLICANT: Dublin, Adrienne B

; APPLICANT: Erlanger, Mark G

; APPLICANT: Huvar, Arne

; APPLICANT: Huvar, Rene

; APPLICANT: Buehler, Lukas K

; TITLE OF INVENTION: DNA Encoding A Human Subunit 5-HT3-C of the 5-HT3 Serotonin Recept

; FILE REFERENCE: ORT-1039

; CURRENT APPLICATION NUMBER: US/09/388,349

; CURRENT FILING DATE: 1999-09-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 9

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-388-349-9

Query Match 100.0%; Score 2360; DB 2; Length 447;

Best Local Similarity 100.0%; Pred. No. 9.5e-238;

Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGGWPARGALLCLTVSLLQQRGDAFTNCSGFDQHGVDPAVQAVFQKAPRPFTNY 60

Db 1 MEGGWPARGALLCLTVSLLQQRGDAFTNCSGFDQHGVDPAVQAVFQKAPRPFTNY 60

Qy 61 SIPTRVNISFTLSAILGVDAQLQLLSFLWMDLVNDPFIWNNPKVCVGINKLTVLAENL 120

Db 61 SIPTRVNISFTLSAILGVDAQLQLLSFLWMDLVNDPFIWNNPKVCVGINKLTVLAENL 120

Qy 121 WLDPDIFVESMDVDPSPGLTAVISSSEGRIKYDKPMRVTSTICNLIDIFYFPDQNCFTTF 180

Db 121 WLDPDIFVESMDVDPSPGLTAVISSSEGRIKYDKPMRVTSTICNLIDIFYFPDQNCFTTF 180

Qy 181 SSFLYTVDSMLLGNQKVEWEITDTSRKVIQTQGEWELLGINKATPKVMGNLNLDQIMFY 240

Db 181 SSFLYTVDSMLLGNQKVEWEITDTSRKVIQTQGEWELLGINKATPKVMGNLNLDQIMFY 240

Qy 241 VATERPSLYIINLLVPSSFVAIDALSFLYLPAESNRAPFKITLLIGYNNVFLMMNDLL 300

Db 241 VATERPSLYIINLLVPSSFVAIDALSFLYLPAESNRAPFKITLLIGYNNVFLMMNDLL 300

Qy 301 PASGTPLISVYFALCLSLMVVSLLETFTYLLHVATTQPPMPRWLHSLLLHCTSPGRC 360

Db 301 PASGTPLISVYFALCLSLMVVSLLETFTYLLHVATTQPPMPRWLHSLLLHCTSPGRC 360

Qy 361 CPTAPQKNGKGLGLTLTHLPKPEKPELAGKGLGPRTEPDGSGWTKTQLMELWQFSH 420
Db 361 CPTAPQKNGKGLGLTLTHLPKPEKPELAGKGLGPRTEPDGSGWTKTQLMELWQFSH 420
Qy 421 AMDTLLRLYLLFWASSILTVILWNT 447
Db 421 AMDTLLRLYLLFWASSILTVILWNT 447

RESULT 2

US-09-579-250-4
; Sequence 4, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent
; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-579-250-4

Query Match 30.4%; Score 717.5; DB 2; Length 457;
Best Local Similarity 35.3%; Pred. No. 4.9e-66;
Matches 155; Conservative 94; Mismatches 141; Indels 49; Gaps 10;

Qy 51 RKAFRPPTNYSIPTRVNSISFTLSAILGVDQALQLLTSFLMMDLVWNPFFNNWPKCEVGI 110
Db 20 KKGVRPVRDWRKPTVSDIVIMTALNVNDEKQVLTYYIWRQYWTDEFLQWTPEDFDNV 79
Qy 111 NKLTVAENLWLPDIFVIESMDVDTSPGLTAYISSEGRKIKYDKPMRVTSICNLDIFYPP 170
Db 80 TKLSIPTDSIWWPDILINEFVDVGKSPNTPYVYVHRGEVQNYKPLQVLTACSLDIYNFP 139
Qy 171 FDOQCTFTFSSFLYTVDSMLGMDKEVMEITDTSRKVIOTQGEWELLGINKATPKMSMG 230
Db 140 FVQNCSLFTSWLHIQDINILWRSPEVR-SDKSIFINQGEWELLEVPQKFSID 198
Qy 231 -NNLYDQIMFYAIRRRPSLYIINLVPSFLVAIDALSFLPAESNRAPPKFTITLLGY 289
Db 199 ISNSYAEMKFYVIRRRPLFYAVSLLPLSIFLWVDIVGFCPLPDSGERVSFKITLLGY 258
Qy 290 NVFLLMMDLLPAS-GTPLISVYFALCLSLMVVSLLETVPITVLLHVATTQPPMPRWLH 348
Db 259 SVFLIIIVSDTLPATIGTPLIGVYFVCMALLVSLAETTFIVRLVHKQDLQ-RPVPDWLR 317
Qy 349 SLLHL-----C--TSPGRCCPTAPOKGNK-----GLGLTLTHLPKPEKPEL- 388
Db 318 HLVLDRIAMWLCGEQPMARPPATFOANKYDCCSGSLLDPAMGNHCHSVGGQDLEKTP 377
Qy 389 --AGKGLGPRETEPDGSGWTKTQLMEL-----WVQFSHAMDTLLF 427
Db 378 RGRGSLPP----PREASLAVRGLLQELSSIRHFLEKRDREVRDMLRGVGVLDRLLF 433
Qy 428 RYLLFWASSILTVILWNT 446
Db 434 RIYLLAVLAYSITLVTLWS 452

RESULT 3

US-09-579-250-6
; Sequence 6, Application US/09579250
; Patent No. 6693172
; GENERAL INFORMATION:
; APPLICANT: Groppi, Vincent

; APPLICANT: Wolfe, Mark L.
; APPLICANT: Berkenpas, Mitchell B
; TITLE OF INVENTION: Methods and Compositions for Measuring Ion Channel
; FILE REFERENCE: FLIPR --Receptor Agonists/Antagonists
; CURRENT APPLICATION NUMBER: US/09/579,250
; CURRENT FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human/mouse
; OTHER INFORMATION: hybrid sequence
US-09-579-250-6

Query Match 24.7%; Score 583.5; DB 2; Length 470;
Best Local Similarity 33.2%; Pred. No. 5.2e-52;
Matches 152; Conservative 73; Mismatches 162; Indels 71; Gaps 15;

Qy 46 QAVFDRKAP-----RPFTNYSIPTRVNSISFTLSAILGVDQALQLLTSFLMMDLV 94
Db 22 QGEFQKLYKELVKYNPLERPVANDSQPLTVYFSLSLQLQIMDVDEKQVLTNTNWLQMS 81
Qy 95 WDNPPFINWPKCEVGINLTVLAENLWLPDIFVIESMD--VDOTPSGLTAYISSEGRIKY 152
Db 82 WTDHYLQMNVSYPGVKTVRFPDQGIWKPDILLYNSADERFDAT-FHTNVLVNSSGHCQY 140
Qy 153 DKPMRVTSICNLDIFYPPDQDQCTFTFSSFLYTVDSMLGMDKEVMEITDTSRKVIQTQ 212
Db 141 LPGIFKSSCYIDVRFPFDVQCKLKFGSWSVGGSLDLQMQE-----ADISGYI--PN 193
Qy 213 GEWELGI--NKATPKMSMGNLYDQIMFYAIRRRPSLYIINLVPSFLVAIDALSFY 270
Db 194 GEWDLVIGPKRSERFECCKEYPDVTFTVIRRRP-FYAVSLLPLSIFLWVDIVGFC 252
Qy 271 LPAESNRAPPKFTITLLGYNVFLMMDLLPAS-GTPLISVYFALCLSLMVVSLLETVFI 329
Db 253 LPDPSGERVSFKITLLGYSVFLIIVSDTLPATIGTPLIGVYFVCMALLVSLAETIFI 312
Qy 330 TVLLHVATTQPPMPRWLHSLHL-----C--TSPGRCCPTAPOKGNK----- 370
Db 313 VRLVHKQDLQ-RPVPDWLRHLVLDRIAWLCLGGEQPMARPPATFOANKYDCCSGSLLP 371
Qy 371 GLGLTLTHLPKPEKPEL---AGKGLGPRETEPDGSGWTKTQLMEL----- 414
Db 372 AMGNHCHSVGGQDLEKTPRGRGSLPP----PREASLAVRGLLQELSSIRHFLEKRD 427
Qy 415 -----WVQFSHAMDTLLRLYLLFWASSILTVILWNT 446
Db 428 REVARDMLRGVGVLDRLFLYLLAVLAYSITLVTLWS 465

RESULT 4

US-09-061-154-2
; Sequence 2, Application US/09061154
; Patent No. 6462188
; GENERAL INFORMATION:
; APPLICANT: Kirkness, E.
; TITLE OF INVENTION: NEW HUMAN 5-HT3 RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 09:05:03 ; Search time 188 Seconds
(without alignments)
1044.693 Million cell updates/sec

Title: US-10-661-378-9
Perfect score: 2360
Sequence: 1 MEGWPARGSALICLTVSL.....RLYLLFMASILLTVILWNT 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2360	100.0	447	4 AAB47151	Aab47151 Human 5-H
2	2348	99.5	447	8 ADM43152	Adm43152 Human 5HT
3	2348	99.5	447	9 AEC01774	Aec01774 Human 5HT
4	1807.5	76.6	456	6 ABU97389	Abu97389 Human ion
5	1787.5	75.7	471	6 ABU97387	Abu97387 Human ion
6	1787.5	75.7	586	4 AAE10121	Aae10121 Human ion
7	1787.5	75.7	586	6 ABU97383	Abu97383 Amino aci
8	1787.5	75.7	586	7 ADE29302	Ade29302 Novel hum
9	1787.5	75.7	614	6 ABU97386	Abu97386 Amino aci
10	1786.5	75.7	471	5 AAU75904	Aau75904 Novel hum
11	1585	67.2	333	4 AAB83413	Aab83413 Human ion
12	1424	60.3	332	4 AAE10122	Aae10122 Human ion
13	1424	60.3	332	6 ABU97382	Abu97382 Amino aci
14	1424	60.3	332	7 ADE29303	Ade29303 Novel hum
15	1036	43.9	267	5 ABP53082	Abp53082 Human TCH
16	996	42.2	192	5 ABP53083	Abp53083 Human TCH
17	975.5	41.3	357	5 AAU75905	Aau75905 Novel hum
18	766	32.5	478	5 ABB08137	Abb08137 Human 5-h
19	766	32.5	478	5 AAU79383	Aau79383 Human 5-h
20	766	32.5	478	7 ADB80480	Adb80480 Ovarian c
21	766	32.5	478	7 ADE62796	Ade62796 Human Pro
22	766	32.5	478	7 ADE61993	Ade61993 Human Pro
23	766	32.5	478	7 ADE62792	Ade62792 Human Pro
24	766	32.5	478	7 ADE56238	Ade56238 Human Pro

25	766	32.5	478	7 ADE61997	Ade61997 Human Pro
26	766	32.5	478	8 ADJ78509	Adj78509 Human 5HT
27	766	32.5	478	8 ADM43151	Adm43151 Human 5HT
28	766	32.5	478	8 ADL82833	Adl82833 Human PRO
29	766	32.5	478	8 ADO05712	Ado05712 Human 5-h
30	766	32.5	478	9 ADX26246	Adx26246 Novel cel
31	766	32.5	519	9 AEC01799	Aec01799 5HT3a wit
32	737.5	31.2	483	9 AEC01773	Aec01773 Human 5HT
33	731.5	31.0	483	7 ADE61991	Ade61991 Rat Prote
34	731.5	31.0	483	7 ADE56236	Ade56236 Rat Prote
35	731.5	31.0	483	7 ADE61995	Ade61995 Rat Prote
36	731.5	31.0	483	8 ADM43149	Adm43149 Rat 5HT3
37	731.5	31.0	483	9 AEC01771	Aec01771 Rat 5HT3
38	729.5	30.9	477	9 ADX26390	Adx26390 Novel cel
39	729.5	30.9	477	9 AEC01579	Aec01579 Rat 5-hyd
40	727	30.8	483	8 ADJ78510	Adj78510 Mouse 5HT
41	717.5	30.4	457	4 AAB50013	Aab50013 Murine 5H
42	717.5	30.4	487	8 ADM43150	Adm43150 Mouse 5HT
43	717.5	30.4	487	9 ADX26318	Adx26318 Novel cel
44	717.5	30.4	487	9 AEC01772	Aec01772 Mouse 5HT
45	717	30.4	740	8 ADK68027	Adk68027 Yellow fl

ALIGNMENTS

RESULT 1
AAB47151
ID AAB47151 standard; protein; 447 AA.
XX
AC AAB47151;
XX
DT 04-JUN-2001 (first entry)
XX
DE Human 5-HT3-C.
XX
KW Human; 5-HT3-C; serotonin; 5-HT3-A receptor; nausea; depression; ulcer;
KW anxiety; psychosis; schizophrenia; urinary continence; anorexia;
KW Huntington's chorea; tardive dyskinesia; Parkinson's disease; allergy;
KW obesity; hypertension; migraine; Gilles de la Tourette's syndrome;
KW sexual dysfunction; drug addiction; Alzheimer's disease; hyperglycemia;
KW cerebral coma; senile dementia; obsessive-compulsive behavior; asthma;
KW panic attack; eating disorder; non-insulin dependent diabetes mellitus;
KW constipation; arrhythmia; stress; inflammation; prostate dysfunction.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 163
FT Misc-difference /note= "Encoded by AAA"
FT Misc-difference 405
FT Misc-difference /note= "Encoded by GCA"
W0200116297-A1.
08-MAR-2001.
14-AUG-2000; 2000WO-US022271.
01-SEP-1999; 99US-00388349.
(ORTH) ORTHO-MCNEIL PHARM INC.
Dubin AE, Erlander MG, Huvar A, Huvar R, Buehler LK;
WPI; 2001-244402/25.
N-PSDB; AAC85574.
New DNA molecule encoding human 5-HT3-C protein for modifying the
function of a serotonin 5-HT3-A receptor.
Claim 11; Fig 3; 78pp; English.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 09:08:53 ; Search time 40 Seconds
(without alignments)
1075.222 Million cell updates/sec

Title: US-10-661-378-9
Perfect score: 2360
Sequence: 1 MEGGWPARQSALLCLTVSLL.....RLYLFPMASSILTVIVLWNT 447
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	722	30.6	462	2 I58179	SHT3 receptor subu
2	717	30.4	489	2 S41757	5-hydroxytryptamin
3	446.5	18.9	464	2 A33523	nicotinic acetylch
4	435	18.4	528	1 ACCH2N	nicotinic acetylch
5	426	18.1	495	2 S60589	acetylcholine rece
6	422	17.9	499	2 A24572	nicotinic acetylch
7	419	17.8	503	2 A53956	nicotinic acetylch
8	417.5	17.7	479	2 A55382	nicotinic acetylch
9	417	17.7	494	2 T09289	nicotinic acetylch
10	414	17.5	455	2 A55972	nicotinic acetylch
11	408	17.3	502	2 A37040	nicotinic acetylch
12	407	17.2	512	2 B37014	nicotinic acetylch
13	406.5	17.2	622	1 ACCH4N	nicotinic acetylch
14	404.5	17.1	511	2 A40110	nicotinic acetylch
15	403	17.1	423	2 T38056	nicotinic acetylch
16	401	17.0	455	2 S51193	nicotinic acetylch
17	400.5	17.0	462	2 S06893	nicotinic acetylch
18	400.5	17.0	627	2 JC4021	nicotinic acetylch
19	399.5	16.9	502	1 ACHUA7	nicotinic acetylch
20	398.5	16.9	501	2 A25338	nicotinic acetylch
21	397.5	16.8	502	2 JN0113	nicotinic acetylch
22	397	16.8	625	2 A26456	nicotinic acetylch
23	395.5	16.8	505	2 S07227	nicotinic acetylch
24	394	16.7	466	2 S16333	nicotinic acetylch
25	393.5	16.7	502	2 G02259	alpha 7 neuronal n
26	392.5	16.6	502	2 A57175	nicotinic acetylch
27	392.5	16.6	502	2 T01378	nicotinic receptor
28	391	16.6	502	2 S10505	nicotinic acetylch
29	389.5	16.5	454	2 B39218	nicotinic acetylch

RESULT 1
I58179
SHT3 receptor subunit - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C:Accession: I58179
R:isenberg, K.E.; Ukhun, I.A.; Holstad, S.G.; Jafri, S.; Uchida, U.; Zorumski, C.F.; Yang Neuroreport 5, 121-124, 1993
A:Title: Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor subunit.
A:Reference number: I58179; MUID:94154206; PMID:7509203
A:Accession: I58179
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-462 <RES>
A:Cross-references: UNIPARC:UPI0000170C0B; EMBL:U01227; NID:g402245; PIDN:AAA52182.1, PII C:Superfamily: acetylcholine receptor

Query Match 30.6%; Score 722; DB 2; Length 462;
Best Local Similarity 35.5%; Pred. No. 4.7e-51;
Matches 153; Conservative 96; Mismatches 144; Indels 38; Gaps 9;

QY	51	RKAPRFTNYSIPTRVNI	SFTLSAILGVDAQLQLTSFLMMDLVNDPFINNPKCVGI	110
DB	30	KGVRVDRWRKPTLSID	VMYAILNVDKQNQLTYIWRQFTDDEFLQWTPEDPDNV	89
QY	111	NKLTVLAENLWLPDIF	VESMDVDQTPSGLTAYISSEGRIKYDKPMRVTSICNLDIFYFP	170
DB	90	TKLSIFDTSIWVDDIL	NEFVDVGKSPSPYVYVHQGEVQNYKPLQVLTACSLDIYNFP	149
QY	171	FDQONCTFTFSFLYTV	DSMLGMKXWEITDTSRKVIQTQGEWELLGINKATPKMSM-	229
DB	150	FDVQNCSLFTSLWHT	IQDINISLWRTPEVR-SDKSIFINQGEWELLGVFTKQFESIE	208
QY	230	GNNLYDQIMFYVAIR	RRPSLIYINLVPSFLVAIDALSFLPAESNRAFPKTLILGY	289
DB	209	TNSYAEKMFYVIRRR	PLFYAVSLSPISFLMVNDIVGFCPLPDGSGERVSFKITLLGY	268
QY	290	NVFLMMNDLLPASG-	-TPLISVYPALCLSLMVVSLETFVITYLLHVAQTQPPMPRWL	347
DB	269	SVFLIIVSDTLPAT	RTPLIGVYFVVCVALLVISLAETIFVQLVHKQDLQ-RPVPDWL	327
QY	348	HSLLH-----C-	-TSPGRCCPTAPQGNK-----GLGLTLTHLPKPKPGBGLAGKLG	394
DB	328	RHLVLDRIAWLLC	LGEGQPMARPPATFQANKTDDCSAMGNHCSHVSPQDLEKTSRSDS	387
QY	395	PRETEPDGSGGWTK	QTMEL-----WQFSHAMDTLLFLYLLFMA	435
DB	388	PL-PPPREASLAVR	GLLQELSSIRHSLEKRDENREVARDWLVGYVLDRLFLFYLLAVL	446
QY	436	SSILTVIVLWN	446	
DB	447	AYSITLVTLWS	457	

ALIGNMENTS

RESULT 2

S41757
5-hydroxytryptamine-3 receptor - mouse
N;Alternate names: serotonin-gated ion channel 5HT3
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S41757; S43205; S48111; S45019; S45020; A40832; I48229; I48230
R;Detz, P.; Abdelaty, F.; Villarroel, A.; Rappold, G.; Weiss, B.; Koenen, M.
PEBS Lett. 339, 302-306, 1994
A;Title: Organisation of the murine 5-HT(3) receptor gene and assignment to human chromosome 10
A;Reference number: S41757; MUID:94156052; PMID:8112471
A;Accession: S41757
A;Molecule type: DNA
A;Residues: 1-489 <UET1>
A;Cross-references: UNIPROT:P3979; UNIPARC:UPI00001779AA; EMBL:Z22772
A;Note: the authors translated the codon TAC for residue 142 as His, GTG for residue 143
R;Detz, P.
submitted to the EMBL Data Library, May 1993
A;Reference number: S43205
A;Accession: S43205
A;Molecule type: DNA
A;Residues: 1-30, 'E', 33-303, 305-311, 'I', 313-385, 'T', 387-489 <UET2>
A;Cross-references: UNIPARC:UPI00001779AB; EMBL:Z22772
R;Hope, A.G.; Downie, D.L.; Sutherland, L.; Lambert, J.J.; Peters, J.A.; Burchell, B.
Eur. J. Pharmacol. 245, 187-192, 1993
A;Title: Cloning and functional expression of an apparent splice variant of the murine 5-HT(3) receptor
A;Reference number: S48111; MUID:93259238; PMID:7683998
A;Accession: S48111
A;Molecule type: DNA
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Title: Preliminary
A;Residues: 1-74, 'V', 76-384, 391-489 <HOP>
A;Cross-references: UNIPARC:UPI000016CB9; EMBL:X72395; NID:g313863; PIDN:CAA51089.1; PIDN:CAA55870.1; PIDN:CAA55871.1; PIDN:CAA55872.1
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1993
R;Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundström, K.; Buell, G.; Humbert, Y.;
submitted to the EMBL Data Library, May 1994
A;Description: Organization of the mouse 5HT3 receptor gene and functional expression of the 5HT3 receptor
A;Reference number: S45019
A;Accession: S45019
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394, 'T', 396-489 <WER>
A;Cross-references: UNIPARC:UPI000016CB9A; EMBL:X79283; NID:g488693; PIDN:CAA55870.1; PIDN:CAA55871.1; PIDN:CAA55872.1
A;Accession: S45020
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384, 391-394, 'T', 396-489 <WE2>
A;Cross-references: UNIPARC:UPI000016CB9B; EMBL:X79283; NID:g488693; PIDN:CAA55871.1; PIDN:CAA55872.1
R;Maricq, A.V.; Peterson, A.S.; Brake, A.J.; Myers, R.M.; Julius, D.
Science 254, 432-437, 1991
A;Title: Primary structure and functional expression of the 5HT-3 receptor, a serotonin-gated ion channel
A;Reference number: A40832; MUID:92022603; PMID:1718042
A;Accession: A40832
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7, 'G', 8-30, 'E', 33-303, 305-489 <MAR>
A;Cross-references: UNIPARC:UPI00001779AC; GB:M74425
R;Werner, P.; Kawashima, E.; Reid, J.; Hussy, N.; Lundström, K.; Buell, G.; Humbert, Y.;
Brain Res. Mol. Brain Res. 26, 233-241, 1994
A;Title: Organization of the mouse 5-HT3 receptor gene and functional expression of two splice variants
A;Reference number: I48229; MUID:95151718; PMID:7854052
A;Accession: I48229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-384, 391-394, 'T', 396-489 <RES>
A;Cross-references: UNIPARC:UPI000016CB9B; EMBL:X79283; NID:g488693; PIDN:CAA55871.1; PIDN:CAA55872.1
A;Accession: I48230
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-394, 'T', 396-489 <RE2>
A;Cross-references: UNIPARC:UPI000016CB9A; EMBL:X79283; NID:g488693; PIDN:CAA55870.1; PIDN:CAA55871.1; PIDN:CAA55872.1
C;Genetics:

A;Introns: 23/1; 78/3; 93/3; 130/2; 187/1; 240/3; 311/1; 385/1

C;Superfamily: acetylcholine receptor
C;Keywords: alternative splicing; ion channel; neurotransmitter receptor; transmembrane I
F;247-273/Domain: transmembrane #status predicted <TM1>
F;279-297/Domain: transmembrane #status predicted <TM2>
F;308-326/Domain: transmembrane #status predicted <TM3>
F;467-486/Domain: transmembrane #status predicted <TM4>

Query Match 30.4%; Score 717; DB 2; Length 489;

Best Local Similarity 35.2%; Pred. No. 1.3e-50;

Matches 155; Conservative 94; Mismatches 141; Indels 50; Gaps 10;

QY 51 RKAFRPTNYSPTRVNIISFTLSAILGVDQAQLQLTSFLMMDLVNDPFINNPKKCVGI 110

DB 51 KKGVRPVRDWRKPTTYSIDVIMVAILNVDEKNQVLTYYWYQYWDTEFLQWTFDFNV 110

QY 111 NKUTVLAENLWLPDIFVSMVDQPPSGLTAVISSEGRKDYDKPMRVTSICMLDIFYPF 170

DB 111 TKLSIPTDSIIVBDILINBFDVGKSPNIPYVYVHRGEVQYKPLQLVTACSLDIYNFP 170

QY 171 FDOONCTFTSSPLXTVDSMLLGMDEKVEITDTSKVIQTQGEWELLGINKATPKMSG 230

DB 171 FDQNCSLFTSWLHTIQDINITLWRSPEVR-SDKSIFINQGEWELLEVPQFKFSID 229

QY 231 -NNLYDQIMFYVAIRRRPSLYIINLVPSSFVAIDALSFLPAESENRAFPKITLLGY 289

DB 230 ISNSYAEMKFYIIRRRPLFYAVALLPSIFLMMVDIVGFCPLPPDSGERVSPKITLLGY 289

QY 290 NVPLMMNDLLPAS--GTPILSVFALCLSLMVVSLLETFTYLLHVATTPPMRWL 347

DB 290 SVFLIIVSDTLPATAGTFLIGYFVYVCMALLVISAETIFIVRLVHKQDLQ-RPVDPDL 348

QY 348 HSLLLH-----C--TSPGRCCPTAPQKNK-----GLGLTTLHLPGKPEGL 388

DB 349 RHVLDRIAMILCLGQPAHRRPAPATQANKTDCSGDLLPAMGNHCVGPGQLEKT 408

QY 389 ---AGKGLGRETEPDGGSGWTNTQLMEL-----WVQFSHAMDTLL 426

DB 409 PRGRGSPLPF---PREASLAVRGLLQELSSIRHFLKREDEMRVADWLRVGYVLDRL 464

QY 427 FRLYLLFMASILTIVLWN 446

DB 465 FRIYLLAVLAYSITLVLWS 484

RESULT 3

A33523

nicotinic acetylcholine receptor beta-3 chain precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 09-Jul-2004

C;Accession: A33523

R;Deneris, E.S.; Boulter, J.; Swanson, L.W.; Patrick, J.; Heinemann, S.

J. Biol. Chem. 264, 6268-6272, 1989

A;Title: Beta-3: a new member of the nicotinic acetylcholine receptor gene family is expressed

A;Reference number: A33523; MUID:8917926; PMID:2703489

A;Accession: A33523

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-464 <DEN>

A;Cross-references: UNIPROT:PI2391; UNIPARC:UPI0000125273; GB:J04636; NID:g3298521; PIDN:

C;Superfamily: acetylcholine receptor

C;Keywords: neurotransmitter receptor; transmembrane protein

Query Match

Best Local Similarity 18.9%; Score 446.5; DB 2; Length 464;

Matches 127; Conservative 86; Mismatches 196; Indels 57; Gaps 14;

QY 15 LTVSLLQGRGDAFTINC--SGFDQGVDPAPVQAVFD--RKAFRPTNYSPTRVNIISF 70

DB 9 LVLSATLSGSWTLTATAGLSVAEH--EDALLHLFGQVQKWRPVLNSSDIKYVFL 66

QY 71 TISAILGVDAQQLQLTSFLMMDLVNDPFINNPKKCVGINKLTVLAENLWLPDIFIVES 130

DB 71 TISAILGVDAQQLQLTSFLMMDLVNDPFINNPKKCVGINKLTVLAENLWLPDIFIVES 130

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 09:24:04 ; Search time 167 Seconds
(without alignments)
1118.381 Million cell updates/sec

Title: US-10-661-378-9
Perfect score: 2360
Sequence: 1 MEGWPARQSALLCLTVSLL.....RLVLLFWASSILTVIVLWNT 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2360	100.0	447	3	US-09-955-524-9
2	2360	100.0	447	5	US-10-661-378-9
3	1795	76.1	457	4	US-10-243-475-132
4	1787.5	75.7	471	4	US-10-243-475-121
5	1787.5	75.7	586	3	US-09-802-668-105
6	1787.5	75.7	586	4	US-10-243-475-105
7	1787.5	75.7	614	4	US-10-243-475-119
8	1786.5	75.7	471	3	US-09-899-495-116
9	1585	67.2	393	4	US-10-149-930-50
10	1424	60.3	332	3	US-09-802-668-106
11	1424	60.3	332	4	US-10-243-475-106
12	975.5	41.3	357	3	US-09-899-495-118
13	766	32.5	478	4	US-10-173-999-44
14	766	32.5	478	4	US-10-339-405-3
15	766	32.5	478	5	US-10-684-206-12
16	766	32.5	478	5	US-10-756-149-5336
17	729.5	30.9	477	5	US-10-973-858-12
18	717.5	30.4	457	4	US-10-740-083-4
19	583.5	24.7	470	4	US-10-740-083-6
20	420	17.8	450	3	US-09-795-693-11
21	420	17.8	450	4	US-10-156-239-11
22	420	17.8	450	4	US-10-199-485-11
23	420	17.8	450	4	US-10-312-088-38
24	420	17.8	450	5	US-10-343-903-15
25	420	17.8	450	5	US-10-687-268-38
26	419	17.8	504	4	US-10-349-836-4
27	419	17.8	504	5	US-10-723-860-3689

28	415.5	17.6	494	4	US-10-349-836-10	Sequence 10, Appli
29	415.5	17.6	494	4	US-10-303-198-2	Sequence 2, Appli
30	413	17.5	439	5	US-10-769-085-13	Sequence 13, Appli
31	412.5	17.5	502	4	US-10-740-083-14	Sequence 14, Appli
32	408	17.3	502	4	US-10-157-031-92	Sequence 92, Appli
33	408	17.3	631	3	US-09-941-179A-7	Sequence 7, Appli
34	407.5	17.3	502	4	US-10-740-083-10	Sequence 10, Appli
35	404.5	17.1	502	4	US-10-740-083-12	Sequence 12, Appli
36	404	17.1	458	4	US-10-349-836-16	Sequence 16, Appli
37	404	17.1	458	4	US-10-303-198-4	Sequence 4, Appli
38	402.5	17.1	502	5	US-10-769-085-11	Sequence 11, Appli
39	402.5	17.1	529	4	US-10-349-836-2	Sequence 2, Appli
40	402.5	17.1	529	4	US-10-415-014-702	Sequence 702, App
41	402.5	17.1	529	4	US-10-415-014-704	Sequence 704, App
42	402.5	17.1	529	4	US-10-415-014-705	Sequence 705, App
43	402.5	17.1	529	4	US-10-757-262-86	Sequence 86, Appli
44	402.5	17.1	529	5	US-10-643-795A-112	Sequence 112, App
45	402.5	17.1	529	5	US-10-643-795A-121	Sequence 121, App

ALIGNMENTS

RESULT 1

US-09-955-524-9
; Sequence 9, Application US/09955524
; Patent No. US20020137138A1
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Huvar, Arne
; APPLICANT: Huvar, Rene
; APPLICANT: Ruehler, Lukas K
; TITLE OF INVENTION: DNA ENCODING A HUMAN SUBUNIT 5-HT3-C OF THE 5-HT3 SEROTONIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: ORT-1039
; CURRENT APPLICATION NUMBER: US/09/955,524
; CURRENT FILING DATE: 2001-09-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-524-9

Query Match	100.0%;	Score 2360;	DB 3;	Length 447;
Best Local Similarity	100.0%;	Pred. No. 1.9e-213;		
Matches 447;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEGWPARQSALLCLTVSLLQGRGDAFTINC	SFGDQHGVDPAVFQAVFDRKAFRPFTNY	60
Db	1	MEGWPARQSALLCLTVSLLQGRGDAFTINC	SFGDQHGVDPAVFQAVFDRKAFRPFTNY	60
Qy	61	SIPTRVNISTLSAILGVDAQLQLLSFLWMDLW	NDPFFNNWPKVCVGINKLTVLAENL	120
Db	61	SIPTRVNISTLSAILGVDAQLQLLSFLWMDLW	NDPFFNNWPKVCVGINKLTVLAENL	120
Qy	121	WLPIRIFVMSDMDQTPSGLTAVTSSSGRIKYD	KPMVTSICNLDIFVFPDQNCQCTFF	180
Db	121	WLPIRIFVMSDMDQTPSGLTAVTSSSGRIKYD	KPMVTSICNLDIFVFPDQNCQCTFF	180
Qy	181	SSFLYTVDSMLLGMKEVWEITDTSRKVIQTQGE	WELLGINKATPKVMGNNLYDQIMFY	240
Db	181	SSFLYTVDSMLLGMKEVWEITDTSRKVIQTQGE	WELLGINKATPKVMGNNLYDQIMFY	240
Qy	241	VATRRRPSLYIINLVPSSEFLVAIDALSFYLP	PAESENRAFPKITLLGYNVFLMMDDL	300
Db	241	VATRRRPSLYIINLVPSSEFLVAIDALSFYLP	PAESENRAFPKITLLGYNVFLMMDDL	300
Qy	301	PASGTPPLISVVFALCLSLMVVSLLETFTYLLH	VATTQPPMPRWLHSLHCTSPGR	360
Db	301	PASGTPPLISVVFALCLSLMVVSLLETFTYLLH	VATTQPPMPRWLHSLHCTSPGR	360

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 09:25:03 ; Search time 27 Seconds
(without alignments)
703.433 Million cell updates/sec

Title: US-10-661-378-9
Perfect score: 2360
Sequence: 1 MEGWPARQSALLCTVSL.....RLVLLFWASSILTVIVLWNT 447

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB pep.*
6: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	766	32.5	478	7	US-11-037-829A-4
2	727	30.8	483	7	US-11-037-829A-5
3	529	22.4	495	7	US-11-037-829A-7
4	415.5	17.6	494	7	US-11-122-144-10
5	405	17.2	458	7	US-11-122-144-16
6	402.5	17.1	529	7	US-11-122-144-2
7	400.5	17.0	627	7	US-11-037-829A-1
8	399.5	16.9	502	7	US-11-122-144-12
9	399.5	16.9	627	7	US-11-122-144-6
10	398	16.9	491	7	US-11-037-829A-9
11	391	16.6	502	7	US-11-122-144-14
12	388	16.4	502	7	US-11-037-829A-2
13	373.5	15.8	485	7	US-11-037-829A-11
14	372	15.8	504	7	US-11-122-144-4
15	371.5	15.7	498	7	US-11-037-829A-3
16	371.5	15.7	498	7	US-11-122-144-18
17	360	15.3	468	7	US-11-122-144-8
18	250.5	10.6	481	6	US-10-512-376-5
19	245.5	10.4	459	6	US-10-512-376-6
20	239	10.1	467	6	US-10-512-376-3
21	239	10.1	496	6	US-10-512-376-2
22	229	9.7	487	7	US-11-241-631-13
23	213	9.0	475	7	US-11-241-631-16
24	213	9.0	487	7	US-11-241-631-14
25	213	9.0	506	7	US-11-241-631-15

26	192.5	8.2	497	7	US-11-037-829A-15	Sequence 15, Appl
27	190	8.1	448	7	US-11-241-631-17	Sequence 17, Appl
28	181	7.7	474	7	US-11-037-829A-13	Sequence 13, Appl
29	180.5	7.6	473	7	US-11-169-041-229	Sequence 229, Appl
30	180	7.6	492	7	US-11-037-829A-12	Sequence 12, Appl
31	177	7.5	485	6	US-10-204-029-7	Sequence 7, Appl
32	169.5	7.2	345	7	US-11-188-353-10	Sequence 10, Appl
33	169.5	7.2	345	7	US-11-188-353-4	Sequence 4, Appl
34	169.5	7.2	420	7	US-11-188-353-8	Sequence 8, Appl
35	169.5	7.2	467	7	US-11-188-353-2	Sequence 2, Appl
36	167	7.1	226	6	US-10-512-376-8	Sequence 8, Appl
37	164	6.9	465	7	US-11-037-829A-14	Sequence 14, Appl
38	160	6.8	422	6	US-10-204-029-4	Sequence 4, Appl
39	160	6.8	426	6	US-10-204-029-2	Sequence 2, Appl
40	98.5	4.2	626	7	US-11-188-298-2725	Sequence 2725, Ap
41	97.5	4.1	264	7	US-11-241-631-18	Sequence 18, Appl
42	95.5	4.0	574	6	US-10-518-341-1	Sequence 1, Appl
43	95.5	4.0	574	7	US-11-022-562-214	Sequence 214, App
44	94	4.0	559	7	US-11-087-099-6637	Sequence 6637, Ap
45	94	4.0	559	7	US-11-188-298-17098	Sequence 17098, A

ALIGNMENTS

RESULT 1
US-11-037-829A-4
; Sequence 4, Application US/11037829A
; Publication No. US20050255551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Benchrif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; TITLE OF INVENTION: Nicotinic Receptor Subunits
; FILE REFERENCE: FI03 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-037-829A-4

Query Match 32.5%; Score 766; DB 7; Length 478;
Best Local Similarity 36.0%; Pred. No. 5.9e-65;
Matches 175; Conservative 94; Mismatches 151; Indels 66; Gaps 14;

Qy	9	QSALLCLTSLLLQGRGDAFTINCSGDFQHGVPAPVQAFVD-----RKAFRPFTNYSI 62
Db	6	QQALLALLPTLL-AOGEAR-----SRNTTPALLR-LSDYLLTYRKGVRVRDWRK 57
Qy	63	PTRVNISFTLSAILGVDAQLQLLTSFLWMDLVNDPFINNPKCEVGINKLTVLAENLWL 122
Db	58	PTTVSDIVVAILNVDEKNQVLTIIWYQYQWTFDPLQNPEDFNITKLSIPTDSIW 117
Qy	123	PDIFIVESMDVDTGPSGLTAYISEGRIKYDKPMRVTSICNLIDIFYPFPQOQCTFTFSS 182
Db	118	PDILINEFVDVGKSNIPYVYIRHQGEVQYKPLQVVVTAGSLDIYNFPFVQNGSLFTS 177
Qy	183	FLYTVDSMLGMKWEWETD---TSRKVIQTQGEWELLGINKATPKWSM-GNNLYDQIM 238
Db	178	WLHTIQDINISL-----WRLPEKVKRSRVFMNGEWELLGLVLPYFRFSMESSNYIAEMK 233
Qy	239	FYVAIRRRPLXYINLLVPSSFLVAIDALSFYLPASENRPAPFKITLLGLVNVFLMMD 298
Db	234	FYVVIARRPLFYVVSLLLPISFILMVDIVGYFLPPNSGERVSKITLLGLVNVFLIIVSD 293

```

QY 299 LLPAS--GTPPLISVYFALCLSLMVVSLLETVFITYLLHVATTOPPPMPRWLHSLLLHCTS 356
Db 294 TLPATAIGTPLIGVYFVVCMLLVISLAETIFIVRLVHKQDIQ-QPVPFWLRHLVLERIA 352
QY 357 PGRCC-----PTAPQGNK-----GLGLTLTLHPG-----KEPGELAGKKLGPRETE 399
Db 353 WLLCLREBOSTQRBPATTSQATKTDCSANGNHCSHMGGPQDFEKSPPRDCSPPPPPRE-- 410
QY 400 PDGSGGWTKTQIMEL-----VVQFSHAMDTLLFRLYLLFMASILT 440
Db 411 ---ASLAVCGLLQELSSIRQLEKREIREVARDWLVRGSLVDKLLFHYLLAVLAYSIT 467
QY 441 VIVLWN 446
Db 468 LVMLWS 473

RESULT 2
US-11-037-829A-5
; Sequence 5, Application US/11037829A
; Publication No. US20050255551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Bencherif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; TITLE OF INVENTION: Nicotinic Receptor Subunits
; FILE REFERENCE: T103 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Mouse
US-11-037-829A-5

```

```

Qy 433 FMASSILTVILWN 446
Db 465 AVLAYSITLWLS 478

RESULT 3
US-11-037-829A-7
; Sequence 7, Application US/11037829A
; Publication No. US2005025551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Bencherif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; TITLE OF INVENTION: Nicotinic Receptor Subunits
; FILE REFERENCE: T103 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human nAChR alpha4-mouse 5HT3-FLAG chimera
US-11-037-829A-7

Query Match 22.4%; Score 529; DB 7; Length 495;
Best Local Similarity 29.2%; Pred. No.: 2.5e-42;
Matches 129; Conservative 85; Mismatches 164; Indels 64; Gaps 12

Qy 55 RPTNYSIPTRVNISFTLSAILGVDAQLQLTSLFWMDLVNDPFINNPKKCVGINKLT 114
Db 53 RPNVANSDDVVLVRFLGSIAQLIDYDEKNQMTTNVVKWQEHDKLRWDPADYENVTSIR 112
Qy 115 VLAENLWLPDIFVESMDVDTQSGLT-AVSSSGRIKYDKPMRVTSICNLIDFVFPDQ 173
Db 113 IPSELWRPDLVLYNADGPAVHLTKAHLFDGRVQWTPPAIYKSCSIDVTFPPDQ 172
Qy 174 QNCTFTFSFLYTVDSMLLGMDKEVMEITDSRKVIQ----TQGEWELLGI--NKATPKM 227
Db 173 QNCTMKFGSMTY-----DRAKIDLNVNHSRVDQLDFWESGEWIVDAVGTYNTRKY 223
Qy 228 SMGNLYDQIMFYVAIRRRPSLYINLLVPSSFLVAIDALSFLYPAESENRAPKFTILL 287
Db 224 ECCABIYPDITYAFVIRLPLFTINLIIPCILSLCTVLVFLYLPSSCGEKITICISVLL 283
Qy 288 GYNVFLIMNDLAPAG--NPLISVYPALCLSLMWVSILLETFTYLLHVATQPPMPMR 345
Db 284 SLTVFLLITIEIPSTSLVPLIGVYFVCMALLVISLAETIFIVLVHKDLQ-RVPVD 342
Qy 346 WLHSLLIH-----C--TSGRCCTPAQGNK-----GLGLTTLHPGPKEPG 386
Db 343 WLRLHLVDRLTAWILICLGEQPMARPPATFOANTKDCGSDLLPAMGNHCSHVGGPDDLE 402
Qy 387 EL---AGKKLGIPRETEPDGGSGWTKTOLMEL-----WVQFSHAMDT 424
Db 403 KTRPGRGSLPP-----PREASLAVRGLQLBELSSIRHFLKRDENRVARDWLRVGYLDR 458
Qy 425 LFLRLYLLFMASISLTVILWN 446
Db 459 LFLRYLLAVLAYSITLWLS 480

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2006, 09:05:33 ; Search time 234 Seconds
(without alignments)
1347.740 Million cell updates/sec

Title: US-10-661-378-9

Perfect score: 2360

Sequence: 1 MEGWPARQSALLCLTVSL.....RLYLFPASSILTVILWNT 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2348	99.5	447	2	Q8WX8 HUMAN
2	1777.5	75.3	471	2	Q7Z652 HUMAN
3	1745	73.9	441	2	Q6V707 HUMAN
4	1725	73.1	456	2	Q6V706 HUMAN
5	1191	50.5	454	2	Q70244 HUMAN
6	778.5	33.0	279	2	Q7Z6B3 HUMAN
7	766	32.5	478	1	5HT3R_HUMAN
8	766	32.5	484	2	Q7KZM7 HUMAN
9	738.5	31.3	483	2	Q9N0F4 MUSPF
10	738	31.3	490	1	5HT3R_CAVPO
11	731.5	31.0	483	1	5HT3R_RAT
12	729.5	30.9	477	2	Q62999 RAT
13	720	30.5	483	2	Q8K1F4 MOUSE
14	717.5	30.4	487	1	5HT3R_MOUSE
15	714	30.3	483	2	Q6J1J7 MOUSE
16	628	26.6	457	2	Q4SRT3 TETNG
17	592	25.1	1044	2	Q4RU50 TETNG
18	574.5	24.3	459	2	Q7ZTN5_XENLA
19	560	23.7	445	2	Q4SRT2 TETNG
20	539.5	22.9	437	2	Q9JHJ5 MOUSE
21	526.5	22.3	441	2	Q95264 HUMAN
22	524.5	22.2	437	2	Q9J16 RAT
23	515.5	21.8	228	2	Q4RU51 TETNG
24	450.5	19.1	464	1	ACHB3_MOUSE
25	446.5	18.9	464	1	ACHB3_RAT
26	439.5	18.6	452	1	ACH10 CHICK
27	439.5	18.6	464	2	Q6PW48 RAT
28	436.5	18.5	509	2	Q7T2R3_FUGRU
29	436	18.5	475	2	Q4SPT0 TETNG
30	435	18.4	475	2	Q4S313 TETNG
31	435	18.4	528	1	ACHA2_CHICK

32	434.5	18.4	465	2	Q6WBY6_FUGRU	Q6wby6 fugu rubrip
33	431.5	18.3	503	2	Q4S314_TETNG	Q4s314 tetraodon n
34	428.5	18.2	479	1	ACHA9_HUMAN	Q9ugml homo sapien
35	428.5	18.2	479	2	Q4WSA2_HUMAN	Q4wsa2 homo sapien
36	426.5	18.1	476	2	Q68RJ6_ONCMY	Q68rj6 oncorhynchu
37	426.5	18.1	555	2	Q7T2U0_FUGRU	Q7t2u0 fugu rubrip
38	426	18.1	495	1	ACHA3_BOVIN	Q07263 boe taurus
39	425.5	18.0	513	2	Q7T2R9_FUGRU	Q7t2r9 fugu rubrip
40	425	18.0	550	1	ACH92_ONCMY	Q68rj7 oncorhynchu
41	424.5	18.0	530	2	Q4T0S4_TETNG	Q4t0s4 tetraodon n
42	424.5	18.0	561	2	Q4RIC6_TETNG	Q4ric6 tetraodon n
43	423	17.9	499	1	ACHA3_MOUSE	Q8r4g9 mus musculu
44	423	17.9	499	2	Q8VHH6_MOUSE	Q8vhh6 mus musculu
45	423	17.9	622	2	Q7T2S3_FUGRU	Q7t2s3 fugu rubrip

ALIGNMENTS

RESULT 1

Q8WX8 HUMAN
ID Q8WX8 HUMAN PRELIMINARY; PRT; 447 AA.
AC Q8WX8;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE 5-hydroxytryptamine receptor 3 subunit C.

GN Name=HTR3C;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP TISSUE=lung;

RC NUCLEOTIDE SEQUENCE.

RA Dubin A.E., Erlander M.G., Huvar A., Huvar R., Buehler L.K.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9)

CC family.

DR EMBL; AF459285; AAL66182.1; -; mRNA.

DR HSSP; P02711; IOED.

DR Ensembl; ENSG00000178084; Homo sapiens.

DR HGNC; HGNC:24003; HTR3C.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0045211; C:postsynaptic membrane; IEA.

DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . .; IEA.

DR GO; GO:0005216; F:ion channel activity; IEA.

DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.

DR GO; GO:0006811; P:ion transport; IEA.

DR InterPro; IPR006201; Neur channel.

DR InterPro; IPR006202; Neur_chan_LBD.

DR Pfam; PF02931; Neur_chan_LBD; 1.

DR Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.

DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.

KW Ion transport; Ionic channel; Postsynaptic membrane; Receptor;

KW Transmembrane; Transport.

SQ SEQUENCE 447 AA; 50247 MW; EA8146A2AA2E1D7 CRC64;

Query Match 99.5%; Score 2348; DB 2; Length 447;

Best Local Similarity 99.6%; Pred. No. 1.3e-177;

Matches 445; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEGWPARQSALLCLTVSLLLQGRDAFTINCSCGFQHGVDPAVFQVDFRKAPRPPTNY 60

Db 1 MEGWPARQSALLCLTVSLLLQGRDAFTINCSCGFQHGVDPAVFQVDFRKAPRPPTNY 60

Qy 61 SIPTRNISFTLSAILGVDAQLQLTSLFWMDLVWNPFFINWNPKECVGINKLTVLAENL 120

Db 61 SIPTRNISFTLSAILGVDAQLQLTSLFWMDLVWNPFFINWNPKECVGINKLTVLAENL 120

121 WLPDIFVSMVDQTPSGLTAYISSEGRKIDKPMRVTSICNLDIFYFPFDQONCTFTF 180
 121 WLPDIFVSMVDQTPSGLTAYISSEGRKIDKPMRVTSICNLDIFYFPFDQONCTFTF 180
 181 SSFLYTVDSMLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSGNNLYDQIMFY 240
 181 SSFLYTVDSMLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSGNNLYDQIMFY 240
 241 VAIRRRPSLIYINLLVPSSEFLVAIDALSFYLPAAESENRAFPFKITLLGYNVFLMMNDLL 300
 241 VAIRRRPSLIYINLLVPSSEFLVAIDALSFYLPAAESENRAFPFKITLLGYNVFLMMNDLL 300
 301 PASGTPPLISVYFALCLSLMVVSLETFYTYLLHVATTQPPMPRWLHSLHLLHCTSPGRC 360
 301 PASGTPPLISVYFALCLSLMVVSLETFYTYLLHVATTQPPMPRWLHSLHLLHCTSPGRC 360
 361 CPTAPQKNGKGLGLTLHPGKPEGLAGKLGPRETEPDGSGWTKTQLMELWQFSH 420
 361 CPTAPQKNGKGLGLTLHPGKPEGLAGKLGPRETEPDGSGWTKTQLMELWQFSH 420
 421 AMDTLLFRLLYLLFMASILLTVIVLWNT 447
 421 AMDTLLFRLLYLLFMASILLTVIVLWNT 447

RESULT 2

Q726B2 HUMAN
 ID Q726B2 HUMAN PRELIMINARY; PRT; 471 AA.
 AC Q726B2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 5-hydroxytryptamine serotonin receptor 3E.
 GN Name=HTR3E;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22686529; PubMed=12801637; DOI=10.1016/S0378-1119(03)00503-1;
 RA Niesler B., Frank B., Kapeller J., Rappold G.A.;
 RT "Cloning, physical mapping and expression analysis of the human 5-HT(3) serotonin receptor-like genes HTR3C, HTR3D and HTR3E."
 RL Gene 310:101-111(2003).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.
 CC EMBL; AV159813; AA038167.1; -; mRNA.
 DR Ensembl; ENSG00000186038; Homo sapiens.
 DR HGNC; HGNC:24005; HTR3E.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045211; C:postsynaptic membrane; IEA.
 DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006029; Neu_chan_LBD.
 DR InterPro; IPR000169; Pept_cys_AS.
 DR Pfam; PF02931; Neur_chan_LBD_1.
 DR Pfam; PF02932; Neur_chan_LBD_1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR PROSITE; PS00639; THIOL PROTEASE HTS; UNKNOWN 1.
 KW Ion transport; Ionic channel, Postsynaptic membrane; Receptor;
 KW Transmembrane; Transport.
 SQ SEQUENCE 471 AA; 52870 MW; E51343F693802F5B CRC64;

Query Match 75.3%; Score 1777.5; DB 2; Length 471;

Best Local Similarity 74.2%; Pred. No. 2.3e-132;
 Matches 333; Conservative 44; Mismatches 63; Indels 9; Gaps 1;
 QY 8 RQSAALLCLTVSLLQGRGDAFTINCSPGQHVDPVAFQAVDPKAFRPTNYISITRVN 67
 DB 23 RRVALLHLTHSMSTTGRGVTFITINCSPGQHVDPVAFQAVDPKAFRPTNYISITRVN 82
 QY 68 ISFTLSAIGVDAQLQLTSFLWMDLVWDNPPINWNPKECVGINKLTVLAENLWLPDIFI 127
 DB 83 ISFAMSAIILDVNEQLHLLSSFLWMDLVWDNPPINWNPKECVGINKLTVLAENLWLPDIFI 142
 QY 128 VESMDVDQTPSGLTAYISSEGRKIDKPMRVTSICNLDIFYFPFDQONCTFTFESSFLYTV 187
 DB 143 IELMDVDKTPKGLTAYISSEGRKIDKPMRVTSICNLDIFYFPFDQONCTFTFESSFLYTV 202
 QY 188 DSMGLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSGNNLYDQIMFVVAIRRRP 247
 DB 203 DSMGLGMDKEVWEITDTSRKVIQTQGEWELLGINKATPKMSGNNLYDQIMFVVAIRRRP 262
 QY 248 SLVIINLLVPSSEFLVAIDALSFYLPAAESENRAFPFKITLLGYNVFLMMNDLLPASGTP 307
 DB 263 SLVINLLVPSSEFLVAIDALSFYLPAAESENRAFPFKITLLGYNVFLMMNDLLPASGTP 322
 QY 308 ISVYFALCLSLMVVSLETFYTYLLHVATTQPPMPRWLHSLHLLHCTSPGRCCTAPQK 367
 DB 323 IGVPFALCLSLMVVSLETFYTYLLHVATTQPPMPRWLHSLHLLHCTSPGRCCTAPQK 382
 QY 368 GNGKGLGLTLHPGKPEGLAGKLGPRETEPDGSGWTKTQ-----LMELWQF 418
 DB 383 ENKGPGLTPTLHPGKPEVSAQMGPEPAEALTGGSEWTRAQREHAQKQHSVELWQF 442
 QY 419 SHAMDTLLFRLLYLLFMASILLTVIVLWNT 447
 DB 443 SHAMDTLLFRLLYLLFMASILLTVIVLWNT 471

RESULT 3
 Q6V707 HUMAN
 ID Q6V707 HUMAN PRELIMINARY; PRT; 441 AA.
 AC Q6V707;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 5-HT3c1 serotonin receptor-like protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22959642; PubMed=14597179; DOI=10.1016/S0378-1119(03)00803-5;
 RA Karnovsky A.M., Gotow L.F., McKinley D.D., Piechan J.L., Ruble C.L.,
 RA Mills C.J., Schellin K.A., Slightom J.L., Fitzgerald L.R.,
 RA Benjamin C.W., Roberts S.L.;
 RT "A cluster of novel serotonin receptor 3-like genes on human chromosome 3."
 RL Gene 319:137-148(2003).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel (TC 1.A.9) family.
 CC EMBL; AV349352; AAQ93476.1; -; mRNA.
 DR Ensembl; ENSG00000186038; Homo sapiens.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045211; C:postsynaptic membrane; IEA.
 DR GO; GO:0005230; F:extracellular ligand-gated ion channel acti. . . ; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0030594; F:neurotransmitter receptor activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006029; Neu_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD_1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR PROSITE; PS00639; THIOL PROTEASE HTS; UNKNOWN 1.